Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claim 1. (Currently amended) A method of extracting structural information from a NMR data set for a selected macromolecule in an intact biological compartment wherein said selected macromolecule is labeled with ~~an~~ a NMR-detectable nucleus, such that said NMR-detectable nucleus is present in said selected macromolecule in an amount greater than is naturally abundant in said macromolecule, said method comprising:

(a) contacting said intact biological compartment with radio frequency energy, thereby producing an excited NMR-detectable nucleus;

(b) collecting radio frequency data from said excited NMR-detectable nucleus, thereby producing said NMR data set, and

(c) analyzing said data set to extract said structural information from the NMR data set for said selected macromolecule ~~from said data set~~.

Claim 2. (Currently amended) The method according to claim **1**, wherein said selected macromolecule is overexpressed in said intact biological compartment.

Claim 3. (Currently amended) The method according to claim **1**, wherein said NMR-detectable nucleus is present in an amount detectable by NMR of said intact biological compartment.

Claim 4. (Original) The method according to claim **1**, wherein said selected macromolecule is a member selected from the group consisting of proteins, saccharides, glycoproteins, and nucleic acids.

Claims 5. - 8. (Cancelled)

Claim 9. (Currently amended) The method according to claim **1**, wherein said selected macromolecule is further labeled with deuterium.

Claim 10. (Currently amended) The method according to claim **1**, wherein said intact biological compartment is present in a suspension.

Claim 11. (Original) The method according to claim **1**, wherein said structural information is conformational information.

Claims 12. - 13. (Cancelled)

Claim 14. (Original) The method according to claim **1**, wherein said structural information is for a first conformation of said selected macromolecule and a second conformation of said selected macromolecule.

Claim 15. (Original) The method according to claim **1**, wherein said data set is acquired by a triple resonance NMR method.

Claim 16. (Original) The method according to claim **15**, wherein said triple resonance NMR experiment is a member selected from HSQC and TROSY.

Claim 17. (Currently amended) The method according to claim **1**, wherein said intact biological compartment is prepared by a method comprising:

(a) transforming an unlabeled precursor of said ~~labeled~~ intact biological compartment with a nucleic acid encoding said selected macromolecule, wherein said nucleic acid is operably linked to a promoter non-native to said unlabeled precursor ~~cell~~ of said intact biological compartment, thereby producing a transformed intact biological compartment;

(b) incubating said transformed intact biological compartment in a medium comprising said NMR-detectable nucleus; and

(c) inducing said transformed intact biological compartment, thereby preparing said ~~labeled~~ intact biological compartment.

Claim 18. (Currently amended) The method according to claim 17, further comprising:

(d) inhibiting essentially all transcription in said transformed intact biological compartment, which is under control of promoters native to said unlabeled

precursor of said intact biological compartment, while allowing transcription under control of said non-native promoter to proceed.

Claim 19. (Cancelled)

Claim 20. (Original) The method according to claim **17**, wherein said medium is deuterated.

Claim 21. (Currently amended) The method according to claim **17**, wherein said intact biological compartment is a bacterial cell.

Claim 22. (Original) The method according to claim **17**, wherein the non-native promoter encodes an RNA polymerase that is operable during step (d).

Claim 23. (Original) The method according to claim **17**, wherein the non-native promoter is a phage promoter.

Claim 24. (Currently amended) The method according to claim 18, wherein said inhibiting is caused by administering an inhibitor to said unlabeled precursor of said intact biological compartment in an amount sufficient to cause said inhibiting.

Claim 25. (Original) The method according to claim **24**, wherein said inhibitor is rifampicin.

Claim 26. (Currently amended) The method of claim **1**, wherein ~~said selected macromolecule experiences a local~~ the viscosity inside said intact biological compartment is at least 2 fold greater than the viscosity of pure water, wherein said ~~local~~ viscosity inside said intact biological compartment and said viscosity of said pure water are determined at the same temperature.

Claim 27. (Currently amended) The method of claim **1**, wherein said selected macromolecule is present in said intact biological compartment at a weight percent of up to 0.3% compared to the total weight of said intact biological compartment.

Claim 28. (Currently amended) The method of claim **1**, wherein said selected macromolecule is present in said intact biological compartment at a weight percent of up to 50% compared to the total weight of said intact biological compartment.

Claim 29. (Original) The method of claim **1**, wherein said selected macromolecule has a molecular weight of at least 5 kDa.

Claim 30. (Original) The method of claim **1**, wherein said selected macromolecule has a molecular weight of at least 25 kDa.

Claim 31. (Original) The method of claim **1**, wherein said selected macromolecule has a molecular weight of at least 70 kDa.

Claim 32. (Currently amended) The method of claim **1**, wherein said intact biological compartment is a living cell.

Claim 33. (Currently amended) The method of claim **1**, wherein said intact biological compartment is a cell that has been metabolically arrested.

Claim 34. (Original) The method of claim **1**, wherein said selected macromolecule is expressed from a plasmid.

Claim 35. (Original) The method of claim **1**, using a multidimensional multinuclear method.

Claim 36. (Currently amended) The method of claim **35**, ~~using an HNCA experiment~~ wherein said multidimensional multinuclear method is an HNCA experiment.

Claim 37. (Currently amended) The method of claim **35**, ~~using an HMQC experiment~~ wherein said multidimensional multinuclear method is an HMQC experiment.

Claim 38. (Currently amended) The method of claim **1**, wherein said intact biological compartment is a biological cell.

Claim 39. (Currently amended) The method of claim **38**, wherein said biological cell is a prokaryotic cell.

Claim 40. (Currently amended) The method of claim **39**, wherein said prokaryotic cell is ~~a~~ an *E. coli* cell.

Claim 41. (Currently amended) The method of claim **38**, wherein said biological cell is ~~a~~ an eukaryotic cell.

Claim 42. (Currently amended) The method of claim **41**, wherein said eukaryotic cell is a yeast cell.

Claim 43. (Currently amended) The method of claim **41**, wherein said eukaryotic cell is a mammalian cell.

Claim 44. (Currently amended) The method of claim **43**, wherein said mammalian cell is a human cell.

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Claims 45. - 88. (Cancelled)

Claim 89. (New) The method of claim **1**, wherein said structural information is a representation of a conformation of a selected macromolecule at a resolution sufficient to determine the relative locations of two or more atoms.

1 new matter

Claim 90. (New) The method of claim **1**, wherein said intact biological compartment is not immobilized.

Claim 91. (New) A method of extracting structural information from a NMR data set for a selected macromolecule in an intact biological compartment, wherein said selected macromolecule is labeled with sufficient NMR-detectable nuclei in order to be detectable by an NMR instrument, said method comprising:

(a) contacting said intact biological compartment with radio frequency energy, thereby producing an excited NMR-detectable nucleus;

(b) collecting radio frequency data from said excited NMR-detectable nucleus, thereby producing said NMR data set, and

(c) analyzing said data set to extract said structural information from the NMR data set for said selected macromolecule.

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